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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/573,630ADATE: 04/25/2002
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ENTERED

3 <110> APPLICANT: MERCHANT, JUANITA L.
 5 <120> TITLE OF INVENTION: ACINETOBACTER OUTER MEMBRANE PROTEIN AND GENE SEQUENCE
 6 COMPOSITIONS AND METHODS
 8 <130> FILE REFERENCE: 4100.001700
 10 <140> CURRENT APPLICATION NUMBER: 09/573,630A
 11 <141> CURRENT FILING DATE: 2000-05-17
 13 <150> PRIOR APPLICATION NUMBER: 60/134,399
 14 <151> PRIOR FILING DATE: 1999-05-17
 16 <160> NUMBER OF SEQ ID NOS: 6
 18 <170> SOFTWARE: PatentIn Ver. 2.1
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 1050
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Acinetobacter sp.
 25 <220> FEATURE:
 26 <221> NAME/KEY: CDS
 27 <222> LOCATION: (1)..(1047)
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 31 Met Lys Met Ser Arg Ile Ala Leu Ala Met Leu Val Ala Ala Pro Phe
 32 1 5 10 15
 34 gct gct gca aat gca ggc gta act gtt act ccg ttg atg ttg ggg tac 96
 35 Ala Ala Ala Asn Ala Gly Val Thr Val Thr Pro Leu Met Leu Gly Tyr
 36 20 25 30
 38 act ttt caa gat acc cag cat aac aat aac ggt aat gat ggc gaa ctt 144
 39 Thr Phe Gln Asp Thr Gln His Asn Asn Asn Gly Asn Asp Gly Glu Leu
 40 35 40 45
 42 act agt agt cct gaa tta caa gac gat tta ttc gta ggt gct gct att 192
 43 Thr Ser Ser Pro Glu Leu Gln Asp Asp Leu Phe Val Gly Ala Ala Ile
 44 50 55 60
 46 ggt gtt gaa tta act cct tgg tta ggt ttt gaa gct gaa tat agc caa 240
 47 Gly Val Glu Leu Thr Pro Trp Leu Gly Phe Glu Ala Glu Tyr Ser Gln
 48 65 70 75 80
 50 gta aag ggc gat gtt gac ggt gct gct gaa ggt gca gaa tac aaa ggc 288
 51 Val Lys Gly Asp Val Asp Gly Ala Ala Glu Gly Ala Glu Tyr Lys Gly
 52 85 90 95
 54 caa aat att gca ggt aac ttc tac gca act tct gac gta ttt act ggt 336
 55 Gln Asn Ile Ala Gly Asn Phe Tyr Ala Thr Ser Asp Val Phe Thr Gly
 56 100 105 110
 58 aac tat gac agc aaa gtg aag cca tat atg ctt cta ggt gcg ggt cac 384
 59 Asn Tyr Asp Ser Lys Val Lys Pro Tyr Met Leu Leu Gly Ala Gly His
 60 115 120 125
 62 tac aaa tac gaa ttt gaa ggt gtg cca cgc ggt act cgc ggt aat gaa 432

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63 Tyr Lys Tyr Glu Phe Glu Gly Val Pro Arg Gly Thr Arg Gly Asn Glu
 64 130 135 140
 66 gaa gaa ggt act cta ggt aat gct ggt gtg ggt gca ttc tgg cac atc 480
 67 Glu Glu Gly Thr Leu Gly Asn Ala Gly Val Gly Ala Phe Trp His Ile
 68 145 150 155 160
 70 aac gat gcc tta gcg cta cgt act gaa gct cgt ggt act tac cac ttt 528
 71 Asn Asp Ala Leu Ala Leu Arg Thr Glu Ala Arg Gly Thr Tyr His Phe
 72 165 170 175
 74 gac gaa aaa ttc tgg aac tac aca gca tta gct ggt ctt aat gtt gtt 576
 75 Asp Glu Lys Phe Trp Asn Tyr Thr Ala Leu Ala Gly Leu Asn Val Val
 76 180 185 190
 78 cta ggt ggt cgt ctg aaa cca gct gct cca gta gtt gaa gtt gct cca 624
 79 Leu Gly Gly Arg Leu Lys Pro Ala Ala Pro Val Val Glu Val Ala Pro
 80 195 200 205
 82 gtt gag cct gta act cca gtt gct cca ccg cca caa gag ttg act gaa 672
 83 Val Glu Pro Val Thr Pro Val Ala Pro Pro Pro Gln Glu Leu Thr Glu
 84 210 215 220
 86 gac ctg aac atg gaa ctt cgt gtt ttt ttc gac act aac aaa agc aac 720
 87 Asp Leu Asn Met Glu Leu Arg Val Phe Phe Asp Thr Asn Lys Ser Asn
 88 225 230 235 240
 90 atc aaa gat caa tac aaa cca gaa atc gct aaa gtt gct gag aag cta 768
 91 Ile Lys Asp Gln Tyr Lys Pro Glu Ile Ala Lys Val Ala Glu Lys Leu
 92 245 250 255
 94 gtt gaa tat cca aac gct act gct cgt atc gaa ggt cac act gac aac 816
 95 Val Glu Tyr Pro Asn Ala Thr Ala Arg Ile Glu Gly His Thr Asp Asn
 96 260 265 270
 98 act ggt cca cgt gca cta aac gaa cgt tta tct cta gca cgt gct aac 864
 99 Thr Gly Pro Arg Ala Leu Asn Glu Arg Leu Ser Leu Ala Arg Ala Asn
 100 275 280 285
 102 tct gtt aaa tct tcg ctt gta aat gaa tac aat gtt gat gca tct cgc 912
 103 Ser Val Lys Ser Ser Leu Val Asn Glu Tyr Asn Val Asp Ala Ser Arg
 104 290 295 300
 106 ttg tct act caa ggt ttc gct tgg gat caa ccg att gct gac aac aac 960
 107 Leu Ser Thr Gln Gly Phe Ala Trp Asp Gln Pro Ile Ala Asp Asn Asn
 108 305 310 315 320
 110 act aaa gaa ggt cgt gct atg aac cgt cgt gta ttc gcg aca atc act 1008
 111 Thr Lys Glu Gly Arg Ala Met Asn Arg Arg Val Phe Ala Thr Ile Thr
 112 325 330 335
 114 ggt agc cgt act gtt tta gct gaa caa cca gtt gct caa taa
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 121 <212> TYPE: PRT
 122 <213> ORGANISM: *Acinetobacter* sp.
 124 <400> SEQUENCE: 2
 125 Met Lys Met Ser Arg Ile Ala Leu Ala Met Leu Val Ala Ala Pro Phe
 126 1 5 10 15
 128 Ala Ala Ala Asn Ala Gly Val Thr Val Thr Pro Leu Met Leu Gly Tyr

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129 20 25 30
 131 Thr Phe Gln Asp Thr Gln His Asn Asn Asn Gly Asn Asp Gly Glu Leu
 132 35 40 45
 134 Thr Ser Ser Pro Glu Leu Gln Asp Asp Leu Phe Val Gly Ala Ala Ile
 135 50 55 60
 137 Gly Val Glu Leu Thr Pro Trp Leu Gly Phe Glu Ala Glu Tyr Ser Gln
 138 65 70 75 80
 140 Val Lys Gly Asp Val Asp Gly Ala Ala Glu Gly Ala Glu Tyr Lys Gly
 141 85 90 95
 143 Gln Asn Ile Ala Gly Asn Phe Tyr Ala Thr Ser Asp Val Phe Thr Gly
 144 100 105 110
 146 Asn Tyr Asp Ser Lys Val Lys Pro Tyr Met Leu Leu Gly Ala Gly His
 147 115 120 125
 149 Tyr Lys Tyr Glu Phe Glu Gly Val Pro Arg Gly Thr Arg Gly Asn Glu
 150 130 135 140
 152 Glu Glu Gly Thr Leu Gly Asn Ala Gly Val Gly Ala Phe Trp His Ile
 153 145 150 155 160
 155 Asn Asp Ala Leu Ala Leu Arg Thr Glu Ala Arg Gly Thr Tyr His Phe
 156 165 170 175
 158 Asp Glu Lys Phe Trp Asn Tyr Thr Ala Leu Ala Gly Leu Asn Val Val
 159 180 185 190
 161 Leu Gly Gly Arg Leu Lys Pro Ala Ala Pro Val Val Glu Val Ala Pro
 162 195 200 205
 164 Val Glu Pro Val Thr Pro Val Ala Pro Pro Pro Gln Glu Leu Thr Glu
 165 210 215 220
 167 Asp Leu Asn Met Glu Leu Arg Val Phe Phe Asp Thr Asn Lys Ser Asn
 168 225 230 235 240
 170 Ile Lys Asp Gln Tyr Lys Pro Glu Ile Ala Lys Val Ala Glu Lys Leu
 171 245 250 255
 173 Val Glu Tyr Pro Asn Ala Thr Ala Arg Ile Glu Gly His Thr Asp Asn
 174 260 265 270
 176 Thr Gly Pro Arg Ala Leu Asn Glu Arg Leu Ser Leu Ala Arg Ala Asn
 177 275 280 285
 179 Ser Val Lys Ser Ser Leu Val Asn Glu Tyr Asn Val Asp Ala Ser Arg
 180 290 295 300
 182 Leu Ser Thr Gln Gly Phe Ala Trp Asp Gln Pro Ile Ala Asp Asn Asn
 183 305 310 315 320
 185 Thr Lys Glu Gly Arg Ala Met Asn Arg Arg Val Phe Ala Thr Ile Thr
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 189 340 345
 193 <210> SEQ ID NO: 3
 194 <211> LENGTH: 36
 195 <212> TYPE: DNA
 196 <213> ORGANISM: Artificial Sequence
 198 <220> FEATURE:
 199 <223> OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
 200 OLIGONUCLEOTIDE
 202 <400> SEQUENCE: 3

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263 tctactcaag gtttcgcttg ggatcaaccg attgctgaca acaacactaa agaaggcgt 1560
264 gctatgaacc gtcgtgtatt cgcgacaatc actggtagcc gtactgttt agctgaacaa 1620
265 ccagttgctc aataattcat tattgaacac tcattaaaag gcagctcttc gacctgcttt 1680
266 tttagtctgt atttgactac c 1701

VERIFICATION SUMMARY

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